REMARKS

INTRODUCTION:

In accordance with the foregoing, claims 13 and 24 have been amended. No new matter is being presented, and approval and entry are respectfully requested.

Claims 13-15 and 24-26 are pending and under consideration. Reconsideration is respectfully requested.

ENTRY OF RESPONSE UNDER 37 C.F.R. §1.116:

Applicants request entry of this Rule 116 Response and Request for Reconsideration because:

(a) it is believed that the amendments of claims 13 and 24 put this application into condition for allowance;

(b) the amendments were not earlier presented because the Applicants believed in good faith that the cited prior art did not disclose the present invention as previously claimed; and/or

(c) the amendments place the application at least into a better form for appeal.

The Manual of Patent Examining Procedures sets forth in §714.12 that "[a]ny amendment that would place the case either in condition for allowance or in better form for appeal may be entered." (Underlining added for emphasis) Moreover, §714.13 sets forth that "[t]he Proposed Amendment should be given sufficient consideration to determine whether the claims are in condition for allowance and/or whether the issues on appeal are simplified." The Manual of Patent Examining Procedures further articulates that the reason for any non-entry should be explained expressly in the Advisory Action.

REJECTION UNDER 35 U.S.C. §101:

A. In the Office Action, at pages 2-3, numbered paragraph 2, claims 13-15 were rejected under 35 U.S.C. §101, for the reasons set forth therein. This rejection is traversed and reconsideration is requested.

As suggested by the Examiner, for clarification, the terminology "molecules" has been inserted into claim 1 so that amended claim 1 recites, in part: "A method of analyzing, by a computer processor, three-dimensional structures of sequences of atoms or atomic groups of molecules of substances, including a first structure of a sequence of atoms or an atomic group of a molecule of a first substance expressed by three-dimensional coordinates of elements belonging to a first point set and a second structure of a sequence of atoms or an atomic group

of a molecule of a second substance expressed by three-dimensional coordinates of elements belonging to a second point set, comprising...".

Hence, it is respectfully submitted that the amended independent claim 13 recites a method for extracting and evaluating mutually similar portions in three-dimensional structures of sequences of atoms or atomic groups of molecules of substances.

The Examiner did not appear to note the physical object pointed out in the previous response. The Applicants again respectfully submit that, for example, the following on page 28, lines 5-15, represents a physical object:

> For instance, it is assumed that there are **substances** expressed by a point set $A=\{a_1, a_2, \ldots, a_i, \ldots, a_m\}$ as shown in FIG. 13A and a point set $B=\{b_1, b_2, \ldots, b_j, \ldots, b_n\}$ as shown in FIG. 13B. The elements constituting these **substances** A and B are related to each other as shown in FIG. 13C, and the **substance** B is rotated and moved so that the r.m.s.d value between the corresponding elements is minimized, as shown in FIG. 13D. The r.m.s.d value is obtained in the following equation wherein U denotes a rotation matrix and w_k denote respective weights: ...(emphasis added)

It is respectfully submitted that the Merriam Webster Online dictionary, a copy of which is included herewith for the Examiner's convenience, defines "**substance**" as a "**physical** material from which something is made or which has discrete existence." Hence, it is submitted that a description of a particular physical object is provided in the specification.

Hence, Applicants submit that the method of claims 13-15 is a comparison of positions of sequences of atoms or groups of atoms in molecules to determine if the position of a sequence of atoms or group of atoms of a molecule of a first substance approximates a position of a sequence of atoms or group of atoms of a molecule of a second substance, thus **identifying the unknown target sequence of atoms or group of atoms of a molecule**. It is respectfully submitted that the courts have held: "[T]he mere fact that a claimed invention involves inputting numbers, calculating numbers, outputting numbers, and storing numbers, in and of itself, would not render it nonstatutory subject matter ..." See State Street Bank & Trust Co. v. Signature Financial Group, 47 USPQ2d 1596, 1602 (Fed. Cir. 1998). To be patentable, an algorithm must be applied in a "useful" way. See State Street at 1601.

It is respectfully submitted that identifying an unknown target sequence of atoms or group of atoms of a molecule is a useful process and thus, is a statutory process under 35 U.S.C. §101.

Hence, it is submitted that amended claim 13 is directed to statutory subject matter and thus is patentable under 35 U.S.C. §101. Since dependent claims 14-15 depend from amended independent claim 13, claims 14-15 are submitted to be directed to statutory subject matter and to be patentable under 35 U.S.C. §101 for at least the reasons that amended claim 13 is

directed to statutory subject matter and is patentable under 35 U.S.C. §101.

B. In the Office Action, at pages 3-4, numbered paragraph 3, claims 13-15 and 24-26 were rejected under 35 U.S.C. §101, for the reasons set forth therein. This rejection is traversed and reconsideration is requested.

It appears that Applicants' statement in the response to the previous office action: "With respect to the Examiner's argument that the sets of three-dimensional coordinates are not limited to originate from two different structures, it is respectfully submitted that the selection of coinciding attributes narrows the field of structures so that it is clear to one skilled in the art how to interpret the results of the correspondence comparison," is unclear to the Examiner. Applicants were merely responding to the Examiner's statement "Thus, the sets of three-dimensional coordinates are not limited to originate from two different structures, and the method may represent comparison of different "domains" of the same structure, e.g. of a nucleic acid." It is respectfully submitted that the amendment of claim 13 (see below) clarifies how the structures are compared.

The description of papain and pepsin digestion was provided to illustrate how partial structures may be obtained, the partial structures being recited, for example, in lines 25-35 of page 53 of the specification.

Independent claim 13, and independent claim 24 in similar fashion, have been amended to recite:

A method of analyzing, by a computer processor, three-dimensional structures <u>of sequences of atoms or atomic groups of molecules of substances,</u> including a first structure <u>of a sequence of atoms or an atomic group of a molecule of a first substance</u> expressed by three-dimensional coordinates of elements belonging to a first point set and a second structure <u>of a sequence of atoms or an atomic group of a molecule of a second substance</u> expressed by three-dimensional coordinates of elements belonging to a second point set, comprising:

dividing the second point set into a plurality of subsets each having a size that is determined by the size of the first point set;

generating a combination of correspondence satisfying a restriction condition between the elements belonging to the first point set and the elements belonging to each of the subsets of the second point set from among all candidates for the combination of correspondence; and

calculating a root mean square distance between the elements corresponding in the combination of correspondence generated, ~~and~~

wherein the restriction condition includes a condition such that an attribute value of each

of the elements belonging to the first point set coincides with an attribute value of the corresponding element belonging to the second point set in a candidate for combination of correspondence,

determining if a degree of spatial similarity between the first structure of the sequence of atoms or the atomic group of the molecule of the first substance and the second structure of the sequence of atoms or the atomic group of the molecule of the second substance is greater than or equal to a predetermined threshold degree of similarity; and

outputting a determination, if the degree of spatial similarity between the first structure of the sequence of atoms or the atomic group of the molecule of the first substance and the second structure of the sequence of atoms or the atomic group of the molecule of the second substance is greater than or equal to the predetermined threshold degree of similarity, that a function of the first structure of the sequence of atoms or the atomic group of the molecule of the first substance is substantially equivalent to a function of the second structure of the sequence of atoms or the atomic group of the molecule of the second substance.

With respect to the Examiner's concerns with the potential utility in comparing different molecules, Applicants reiterate that the specification, on page 2, lines 22-29, the specification states: "For instance, a commonly existing sequence pattern (region) is known to be found when the amino acid sequences in **proteins having the same function** are compared between different types of organisms. This region is called a motif. Accordingly, if it is possible to extract the motif automatically, the property and function of the protein can be shown by finding which motif is included in the sequence" (emphasis added). This means that, for example:

1) Target Protein A and known Protein B are being compared, wherein target Protein A is from organism AA, and known Protein B is from a different type of organism BB.

2) The method of the present invention is used to show, for example, that an amino acid sequence in target Protein A has a degree of similarity with a known amino acid sequence in Protein B, wherein the degree of similarity is greater than a predetermined threshold value.

3) The sequence of target Protein A having the degree of similarity greater than the predetermined threshold value is thus a "motif," which is associated with a particular function (known because the known amino acid sequence in Protein B is associated with the motif and function).

4) Hence, the amino acid sequence region of target Protein A is associated with the particular function and motif of the amino acid sequence of known Protein B.

It is respectfully submitted that amended independent claims 13 and 24 thus provide an "immediately useful" result, i.e., a method of determining if a degree of spatial similarity between the first structure of the sequence of atoms or the atomic group of the molecule of the first

substance and the second structure of the sequence of atoms or the atomic group of the molecule of the second substance is greater than or equal to a predetermined threshold degree of similarity, and if so, outputting a determination that a function of the first structure of the sequence of atoms or the atomic group of the molecule of the first substance is substantially equivalent to a function of the second structure of the sequence of atoms or the atomic group of the molecule of the second substance.

Hence, amended independent claims 13 and 24 are submitted to have patentable utility under 35 U.S.C. §101. Since claims 14-15 and 25-26 depend from amended claims 13 and 24, respectively, claims 14-15 and 25-26 are submitted to have patentable utility under 35 U.S.C. §101 for at least the reasons that amended claims 13 and 24, respectively, have patentable utility under 35 U.S.C. §101.

REJECTION UNDER 35 U.S.C. §112:

In the Office Action, at page 4, numbered paragraph 4, claims 13-15 and 24-26 were rejected under 35 U.S.C. §112, first paragraph, for the reasons set forth therein. This rejection is traversed and reconsideration is requested.

As described above, the present invention clearly produces a useful result. FIG. 1 illustrates an embodiment of an apparatus that utilizes the method of the present invention, thus enabling automatic determination of the correspondence/similarity determination with respect to desired molecules, which speeds up the process of such a determination in comparison with a manual determination, which takes a greater amount of time and is unwieldy due to the large amount of data handled.

It is respectfully submitted that the operations of the method are clear to those skilled in the art. The operations of amended claim 13, for example, are set forth below in a table with a brief synopsis of each:

Claim 13	Brief synopsis
A method of analyzing, by a computer processor, three-dimensional structures of sequences of atoms or atomic groups of atoms molecules of substances, including a first structure of a sequence of atoms or an atomic group of a molecule of a first substance expressed by three-dimensional coordinates of elements belonging to a first point set and a second structure of a sequence of atoms or an atomic group of a molecule of a second substance expressed by three-dimensional coordinates of elements belonging to a second point set, comprising:	A computer processor implements a method of analyzing three- dimensional structures of a sequence of atoms or atomic groups of atoms of a target molecule represented by a first point set and of a sequence of atoms or atomic groups of atoms of a known molecule represented by a second point set, the method comprising:

dividing the second point set into a plurality of subsets each having a size that is determined by the size of the first point set;	dividing the second point set into subsets in accordance with the size of the first point set;
generating a combination of correspondence satisfying a restriction condition between the elements belonging to the first point set and the elements belonging to each of the subsets of the second point set from among all candidates for the combination of correspondence; and	generating a combination of correspondence between elements of the first and second set that are candidates for the combination of correspondence based on a restriction condition;
calculating a root mean square distance between the elements corresponding in the combination of correspondence generated,	calculating a rmsd for the elements of the combination of correspondence;
wherein the restriction condition includes a condition such that an attribute value of each of the elements belonging to the first point set coincides with an attribute value of the corresponding element belonging to the second point set in a candidate for combination of correspondence,	wherein the restriction condition includes a condition that attribute values of the elements of the first and second set coincide in a candidate for correspondence;
determining if a degree of spatial similarity between the first structure of the sequence of atoms or the atomic group of the molecule of the first substance and the second structure of the sequence of atoms or the atomic group of the molecule of the second substance is greater than or equal to a predetermined threshold degree of similarity; and	determining if the degree of spatial similarity of the first structure and the second structure is greater than or equal to a predetermined threshold degree of similarity; and
outputting a determination, if the degree of spatial similarity between the first structure of the sequence of atoms or the atomic group of the molecule of the first substance and the second structure of the sequence of atoms or the atomic group of the molecule of the second substance is greater than or equal to the predetermined threshold degree of similarity, that a function of the first structure of the sequence of atoms or the atomic group of the molecule of the first substance is substantially equivalent to a function of the second structure of the sequence of atoms or the atomic group of the molecule of the second substance.	if the degree of spatial similarity of the first structure and the second structure is greater than or equal to the predetermined threshold degree of similarity, outputting a determination that the functions of the sequence of atoms or atomic groups of atoms of the target molecule and of a sequence of atoms or atomic groups of atoms of a known molecule are substantially equivalent.

Amended independent claim 24 is similar to the description set forth above for amended claim 13.

Hence, it is respectfully submitted that one skilled in the art would clearly know how to

use the method of the present invention, as set forth in amended independent claims 13 and 24, which set forth the utility of determining if a degree of spatial similarity between the first structure of the sequence of atoms or the atomic group of the molecule of the first substance and the second structure of the sequence of atoms or the atomic group of the molecule of the second substance is greater than or equal to a predetermined threshold degree of similarity, and if so, outputting a determination that a function of the first structure of the sequence of atoms or the atomic group of the molecule of the first substance is substantially equivalent to a function of the second structure of the sequence of atoms or the atomic group of the molecule of the second substance. Thus, amended independent claims 13 and 24 are submitted to be allowable under 35 U.S.C. §112, first paragraph.

Since claims 14-15 and 25-26 depend from amended independent claims 13 and 24, respectively, claims 14-15 and 25-26 are submitted to be allowable under 35 U.S.C. §112, first paragraph for at least the reasons that amended independent claims 13 and 24 are allowable under 35 U.S.C. §112, first paragraph.

REJECTION UNDER 35 U.S.C. §102:

In the Office Action, at page 5, numbered paragraph 5, claims 13-15 and 24-26 were rejected under 35 U.S.C. §102(b) as being anticipated by U.S. 4,853,871 or Holak et al. or Flaherty et al. or Mosimann et al. This rejection is traversed and reconsideration is requested.

As noted above, independent claims 13 and 24 have been amended for clarity.

It is respectfully submitted that amended claim 13 recites a method of analyzing, by a computer processor, three-dimensional structures of sequences of atoms or atomic groups of molecules of substances, including a first structure of a sequence of atoms or an atomic group of a molecule of a first substance expressed by three-dimensional coordinates of elements belonging to a first point set and a second structure of a sequence of atoms or an atomic group of a molecule of a second substance expressed by three-dimensional coordinates of elements belonging to a second point set, comprising: dividing the second point set into a plurality of subsets each having a size that is determined by the size of the first point set; generating a combination of correspondence satisfying a restriction condition between the elements belonging to the first point set and the elements belonging to each of the subsets of the second point set from among all candidates for the combination of correspondence; and calculating a root mean square distance between the elements corresponding in the combination of correspondence generated, wherein the restriction condition includes a condition such that an attribute value of each of the elements belonging to the first point set coincides with an attribute value of the corresponding element belonging to the second point set in a candidate for

combination of correspondence, determining if a degree of spatial similarity between the first structure of the sequence of atoms or the atomic group of the molecule of the first substance and the second structure of the sequence of atoms or the atomic group of the molecule of the second substance is greater than or equal to a predetermined threshold degree of similarity; and outputting a determination, if the degree of spatial similarity between the first structure of the sequence of atoms or the atomic group of the molecule of the first substance and the second structure of the sequence of atoms or the atomic group of the molecule of the second substance is greater than or equal to the predetermined threshold degree of similarity, that a function of the first structure of the sequence of atoms or the atomic group of the molecule of the first substance is substantially equivalent to a function of the second structure of the sequence of atoms or the atomic group of the molecule of the second substance.

It is respectfully submitted that U.S. 4,853,871 (Pantoliano et al.) recites in claim 1, set for the below for the convenience of the Examiner:

> 1. A computer based method for evaluating a protein's structure to determine whether said protein contains at least two target amino acid residues, **replacement of at least one of which with a cysteine residue would be sufficient to permit formation of at least one potentially protein-stabilizing disulfide bond**; said method comprising the steps:
> (1) examining each selected pair of amino acid residues in said protein to determine if they contain certain atoms whose relative three-dimensional positions possess a geometric conformation similar to a geometric conformation possessed by **atoms of a disulfide bond,**
> (2) examining any pair of amino acids found to contain said certain atoms identified in step (1) to determine whether said disulfide bond can be accommodated without creating **unacceptable steric hindrance**,
> (3) permitting an expert operator (i) to view any possible disulfide bond which can be accommodated without creating unacceptable steric hindrance, and (ii) to rank said viewed possible disulfide bond from most likely to stabilize an engineered protein to least likely **to stabilize said protein**, and
> (4) **evaluating said ranked possible disulfide bond** according to expert rule criterion. (emphasis added)

Thus, as is clear from claim 1 of Pantoliano et al., USPN 4,853,871 recites steps for analyzing disulfide bonds (**not sequence structure**) coupling amino acids and the stability or lack thereof of the protein having same, and does not recite the operations of the amended claims 13 and 24 (see above) of the method of the present invention.

Hence, amended claims 13 and 24 are respectfully submitted not to be anticipated under 35 U.S.C. §102(b) by U.S. 4,853,871. Since claims 14-15 and 25-26 depend from amended claims 13 and 24, respectively, claims 14-15 and 25-26 are submitted not to be anticipated under 35 U.S.C. §102(b) by U.S. 4,853,871 for at least the reasons that amended claims 13 and 24 are not anticipated under 35 U.S.C. §102(b) by U.S. 4,853,871.

Holak et al. discloses determination of a three dimensional structure of the trypsin inhibitor from squash seeds in aqueous solution by **nuclear magnetic resonance** and a **combination of distance geometry and dynamical simulated annealing** (see Abstract, Holak et al.). However, Holak et al. does not recite a method of analyzing, by a computer processor, three-dimensional structures of sequences of atoms or atomic groups of molecules of substances, including a first structure of a sequence of atoms or an atomic group of a molecule of a first substance expressed by three-dimensional coordinates of elements belonging to a first point set and a second structure of a sequence of atoms or an atomic group of a molecule of a second substance expressed by three-dimensional coordinates of elements belonging to a second point set, comprising: dividing the second point set into a plurality of subsets each having a size that is determined by the size of the first point set; generating a combination of correspondence satisfying a restriction condition between the elements belonging to the first point set and the elements belonging to each of the subsets of the second point set from among all candidates for the combination of correspondence; and calculating a root mean square distance between the elements corresponding in the combination of correspondence generated, wherein the restriction condition includes a condition such that an attribute value of each of the elements belonging to the first point set coincides with an attribute value of the corresponding element belonging to the second point set in a candidate for combination of correspondence, determining if a degree of spatial similarity between the first structure of the sequence of atoms or the atomic group of the molecule of the first substance and the second structure of the sequence of atoms or the atomic group of the molecule of the second substance is greater than or equal to a predetermined threshold degree of similarity; and outputting a determination, if the degree of spatial similarity between the first structure of the sequence of atoms or the atomic group of the molecule of the first substance and the second structure of the sequence of atoms or the atomic group of the molecule of the second substance is greater than or equal to the predetermined threshold degree of similarity, that a function of the first structure of the sequence of atoms or the atomic group of the molecule of the first substance is substantially equivalent to a function of the second structure of the sequence of atoms or the atomic group of the molecule of the second substance, as is recited by amended independent claim 13, and similarly by amended independent claim 24, of the present invention.

Thus, amended independent claims 13 and 24 are respectfully submitted not to be anticipated under 35 U.S.C. §102(b) by Holak et al. Since claims 14-15 and 25-26 depend from amended claims 13 and 24, respectively, claims 14-15 and 25-26 are submitted not to be anticipated under 35 U.S.C. §102(b) by Holak et al. for at least the reasons that amended claims 13 and 24 are not anticipated under 35 U.S.C. §102(b) by Holak et al.

Flaherty et al. discloses **using a rmsd and a "fingerprint"** to determine similarity of the

three-dimensional structures of actin and the ATPase fragment of a 70-kDa heat shock cognate protein, noting that the structural differences between the two molecules mainly occur in loop regions of actin known to be involved in interactions with other monomers in the actin filament or in the binding of myosin (see Abstract, Flaherty et al.). However, Flaherty does not recite a method of analyzing, by a computer processor, three-dimensional structures of sequences of atoms or atomic groups of molecules of substances, including a first structure of a sequence of atoms or an atomic group of a molecule of a first substance expressed by three-dimensional coordinates of elements belonging to a first point set and a second structure of a sequence of atoms or an atomic group of a molecule of a second substance expressed by three-dimensional coordinates of elements belonging to a second point set, comprising: dividing the second point set into a plurality of subsets each having a size that is determined by the size of the first point set; generating a combination of correspondence satisfying a restriction condition between the elements belonging to the first point set and the elements belonging to each of the subsets of the second point set from among all candidates for the combination of correspondence; and calculating a root mean square distance between the elements corresponding in the combination of correspondence generated, wherein the restriction condition includes a condition such that an attribute value of each of the elements belonging to the first point set coincides with an attribute value of the corresponding element belonging to the second point set in a candidate for combination of correspondence, determining if a degree of spatial similarity between the first structure of the sequence of atoms or the atomic group of the molecule of the first substance and the second structure of the sequence of atoms or the atomic group of the molecule of the second substance is greater than or equal to a predetermined threshold degree of similarity; and outputting a determination, if the degree of spatial similarity between the first structure of the sequence of atoms or the atomic group of the molecule of the first substance and the second structure of the sequence of atoms or the atomic group of the molecule of the second substance is greater than or equal to the predetermined threshold degree of similarity, that a function of the first structure of the sequence of atoms or the atomic group of the molecule of the first substance is substantially equivalent to a function of the second structure of the sequence of atoms or the atomic group of the molecule of the second substance, as is recited by amended independent claim 13, and similarly by amended independent claim 24, of the present invention.

Thus, amended independent claims 13 and 24 are respectfully submitted not to be anticipated under 35 U.S.C. §102(b) by Flaherty et al. Since claims 14-15 and 25-26 depend from amended claims 13 and 24, respectively, claims 14-15 and 25-26 are submitted not to be anticipated under 35 U.S.C. §102(b) by Flaherty et al. for at least the reasons that amended claims 13 and 24 are not anticipated under 35 U.S.C. §102(b) by Flaherty et al.

Mosimann et al. discloses a comparative molecular model of P-30 protein constructed

based on the known three-dimensional structure of bovine pancreatic RNase, wherein, in the **modeling procedure, automatic sequence alignments were revised based upon** the **inspection of the RNase A structure before the amino acids of the P-30 protein were assigned the coordinates of the RNase A template, intermolecular steric clashes were relieved** on an interactive graphics device through the **adjustment of side chain torsion angles**, and **energy minimizing** of the model to optimize stereochemistry and relieve any remaining unacceptably close contacts (see Abstract, Mosimann et al.). However, Mosimann et al. does not recite a method of analyzing, by a computer processor, three-dimensional structures of sequences of atoms or atomic groups of molecules of substances, including a first structure of a sequence of atoms or an atomic group of a molecule of a first substance expressed by three-dimensional coordinates of elements belonging to a first point set and a second structure of a sequence of atoms or an atomic group of a molecule of a second substance expressed by three-dimensional coordinates of elements belonging to a second point set, comprising: dividing the second point set into a plurality of subsets each having a size that is determined by the size of the first point set; generating a combination of correspondence satisfying a restriction condition between the elements belonging to the first point set and the elements belonging to each of the subsets of the second point set from among all candidates for the combination of correspondence; and calculating a root mean square distance between the elements corresponding in the combination of correspondence generated, wherein the restriction condition includes a condition such that an attribute value of each of the elements belonging to the first point set coincides with an attribute value of the corresponding element belonging to the second point set in a candidate for combination of correspondence, determining if a degree of spatial similarity between the first structure of the sequence of atoms or the atomic group of the molecule of the first substance and the second structure of the sequence of atoms or the atomic group of the molecule of the second substance is greater than or equal to a predetermined threshold degree of similarity; and outputting a determination, if the degree of spatial similarity between the first structure of the sequence of atoms or the atomic group of the molecule of the first substance and the second structure of the sequence of atoms or the atomic group of the molecule of the second substance is greater than or equal to the predetermined threshold degree of similarity, that a function of the first structure of the sequence of atoms or the atomic group of the molecule of the first substance is substantially equivalent to a function of the second structure of the sequence of atoms or the atomic group of the molecule of the second substance, as is recited by amended independent claim 13, and similarly by amended independent claim 24, of the present invention.

Thus, amended independent claims 13 and 24 are respectfully submitted not to be anticipated under 35 U.S.C. §102(b) by Mosimann et al. Since claims 14-15 and 25-26 depend

from amended claims 13 and 24, respectively, claims 14-15 and 25-26 are submitted not to be anticipated under 35 U.S.C. §102(b) by Mosimann et al. for at least the reasons that amended claims 13 and 24 are not anticipated under 35 U.S.C. §102(b) by Mosimann et al.

DOUBLE PATENTING:

In the Office Action, at page 5, numbered paragraph 6, claims 13-15 and 2-26 were rejected under the judicially created doctrine of obvious-type double patenting as being unpatentable over claims 16, 17 or co-pending application 09/909809 or claims 5-11, 24 of co-pending application 09/910,054. The reasons for the rejection are set forth in the Office Action and therefore not repeated. The rejection is traversed and reconsideration is requested.

Since U.S. Patent Application Nos. 09/909,809 and 09/910,054 have not yet been issued as patents, and since the all of the claims of the instant application have not yet been indicated as allowable except for the provisional rejection, it is believed that any submission of a Terminal Disclaimer or arguments as to the non-obvious nature of the claims would be premature. MPEP 804(I)(B). As such, it is respectfully requested that the Applicants be allowed to address any obviousness-type double patenting issues remaining once the rejections of the claims in the present application are resolved or on allowance of U.S. Patent Application Nos. 09/909,809 and 09/910,054

CONCLUSION:

In accordance with the foregoing, it is respectfully submitted that all outstanding objections and rejections have been overcome and/or rendered moot, and further, that all pending claims patentably distinguish over the prior art. Thus, there being no further outstanding objections or rejections, the application is submitted as being in condition for allowance which action is earnestly solicited. At a minimum, this Amendment should be entered at least for purposes of Appeal as it either clarifies and/or narrows the issues for consideration by the Board.

If the Examiner has any remaining issues to be addressed, it is believed that prosecution can be expedited and possibly concluded by the Examiner contacting the undersigned attorney for a telephone interview to discuss any such remaining issues.

If there are any underpayments or overpayments of fees associated with the filing of this Amendment, please charge and/or credit the same to our Deposit Account No. 19-3935.

Respectfully submitted,

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Merriam-Webster Online Dictionary

Thesaurus

substance

7 entries found for **substance**.
To select an entry, click on it.

substance
cytosol
ground substance
queen substance
substance abuse
substance P
Go

Main Entry: **sub·stance**
Pronunciation: 's&b-st&n(t)s
Function: *noun*
Etymology: Middle English, from Middle French, from Latin *substantia,* from *substant-, substans,* present participle of *substare* to stand under, from *sub-* + *stare* to stand -- more at STAND
1 a : essential nature **:** ESSENCE **b :** a fundamental or characteristic part or quality **c** *Christian Science* **:** GOD 1b
2 a : ultimate reality that underlies all outward manifestations and change **b :** practical importance **:** MEANING, USEFULNESS <the... bill--which will be without *substance* in the sense that it will authorize nothing more than a set of ideas -- Richard Reeves>
3 a : physical material from which something is made or which has discrete existence **b :** matter of particular or definite chemical constitution **c :** something (as drugs or alcoholic beverages) deemed harmful and usually subject to legal restriction <possession of a controlled *substance*> <has a *substance* problem>
4 : material possessions **:** PROPERTY <a family of *substance*>
- **sub·stance·less** /-l&s/ *adjective*
- **in substance :** in respect to essentials **:** FUNDAMENTALLY

For More Information on "substance" go to Britannica.com

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Pronunciation Symbols